WHAT IS CLAIMED IS:

1. A method of using a functional cation channel protein in an assay for screening potential drugs or agents which interact with the cation channel protein, the method comprising the steps of:

a) providing a functional cation channel protein;

b) conjugating the functional cation channel protein to a solid phase resin;

c) contacting the potential drug or agent to the functional cation channel protein conjugated to the solid phase resin;

d) removing the functional cation channel protein from the solid phase resin: and

e) determining whether the potential drug or agent is bound to the cation channel protein.

2. The method of Claim 1, wherein the providing step comprises:

a) expressing an isolated nucleic acid molecule encoding the cation channel protein in a unicellular host such that the cation channel protein is present in the cell membrane of the unicellular host;

b) lysing the unicellular host in a solubilizing solution so that the cation channel protein is solubilized in the solution; and

c) extracting the cation channel protein from the solublizing solution with a detergent.

3. The method of Claim 2, wherein lysing the unicellular host in a solubilizing solution comprises sonicating the unicellular host in a solution comprising 50 mM Tris buffer, 100 mM KCl, 10 mM $MgSO_4$, 25 mg DNAse 1, 250 mM sucrose, pepstatin,

leupeptin, and PMSF, pH 7.5.

4. The method of Claim 2, wherein the detergent comprises 40 mM decylmaltoside.

5. The method of Claim 1, wherein the conjugating step comprises binding the cation channel protein to a cobalt resin at protein to resin ratio that allows for saturation of the resin with the cation channel protein.

6. The method of Claim 1, wherein the removing step comprises contacting the cation channel protein conjugated to the solid phase resin to an imidazole solution.

7. The method of Claim 1, wherein the isolated nucleic acid molecule encoding the cation channel protein comprises a DNA sequence of SEQ ID NO:17, or degenerate variants thereof, or an isolated nucleic acid molecule hybridizable under standard hybridization conditions to an isolated nucleic acid molecule comprising a DNA sequence of SEQ ID NO:17, or degenerate variants thereof.

8. The method of Claim 1, wherein the potential drug or agent is a member of a libarary of compounds, and the contacting step comprises contacting the library of compounds to the functional cation channel protein conjugated to the solid phase resin.

9. The method of Claim 8, wherein the library of compounds comprises a mixture of compounds or a combinatorial library.

10. The method of Claim 9, wherein the combinatorial library comprises a phage display library, or a synthetic peptide library.

11. A prokaryotic cation channel protein mutated to mimic a functional eukaryotic cation channel protein.

12. The prokaryotic cation channel protein of Claim 11, selected from the group consisting of a potassium channel protein, a sodium channel protein, or a calcium channel protein.

13. The prokaryotic cation channel protein of Claim 11, endogenously produced in a prokaryotic organism selected from the group consisting of *E.coli*, *Streptomyces lividans*, *Clostridium acetobutylicum*, or *Staphylcoccus aureus*.

14. The prokaryotic cation channel protein of Claim 11, comprising an amino acid sequence of SEQ ID Nos: 1, 2, 3, or 7.

15. The prokaryotic cation channel protein of Claim 11, wherein said prokaryotic cation channel protein is a potassium channel protein from *Streptomyces lividans*.

16. The prokaryotic cation channel of Claim 15, encoded by a nucleic acid comprising a DNA sequence of SEQ ID NO:17, or degenerate variants thereof.

17. The prokaryotic cation channel protein of Claim 15, comprising an amino acid sequence of SEQ ID NO:1, or conserved variants thereof.

18. The prokaryotic cation channel protein of Claim 11, wherein the functional eukaryotic cation channel protein comprises a eukaryotic potassium channel protein, a eukaryotic sodium channel protein, or a eukaryotic calcium channel protein.

19. The prokaryotic cation channel protein of Claim 11, wherein said functional eukaryotic cation channel protein is endogenously produced in a eukaryotic organism comprising insects or mammals.

20. The prokaryotic cation channel protein of Claim 19, wherein said eukaryotic organism comprises *Drosophila melanogaster*, *Homo sapiens*, *C. elegans*, *Mus musculus*, *Arabidopsis thaliana*, *paramecium tetraaurelia* or *Rattus novegicus*.

21. The prokaryotic cation channel protein of Claim 11, mutated to mimic a eukaryotic cation channel protein comprising an amino acid sequence comprising SEQ ID Nos: 4, 5, 6, 8, 9, 10, 11, 12, 13, or 14.

22. The prokaryotic cation channel protein of Claim 21, wherein said prokaryotic channel protein is a potassium channel protein from *Streptomyces lividans* comprising an

amino acid sequence of SEQ ID NO:1, said eukaryotic cation channel is a potassium channel protein comprising an amino acid sequence of SEQ ID NO:4, and said mutated prokaryotic channel protein comprises an amino acid sequence of SEQ ID NO:16, or conserved variants thereof.

23. The prokaryotic cation channel protein of Claim 22, wherein said mutated porkaryotic channel protein is encoded by an isolated nucleic acid molecule comprising a DNA sequence of SEQ ID NO:17, or degenerate variants thereof.

24. An isolated nucleic acid molecule which encodes a mutant K^+ channel protein, comprising a DNA sequence of SEQ ID NO:17, or degenerate variants thereof.

25. An isolated nucleic acid molecule hybridizable to the isolated nucleic acid molecule of Claim 24 under standard hybridization conditions.

26. The isolated nucleic acid molecule of Claim 24, detectably labeled.

27. The isolated nucleic acid molecule of Claim 25, detectably labeled.

28. The detectably labeled isolated nucleic acid molecule of either of Claims 26 or 27, wherein said detectable label comprises radioactive isotopes, compounds which fluoresce, or enzymes.

29. The isolated nucleic acid molecule of either of Claims 24 or 25, which encode a polypeptide comprising an amino acid sequence of SEQ ID NO:16, or conserved variants thereof.

30. An isolated polypeptide comprising an amino acid sequence of SEQ ID NO:16, or conserved variants thereof.

31. An antibody having a polypeptide of Claim 30 as an immunogen.

32. The antibody of Claim 31, wherein said antibody is a monoclonal antibody.

33. The antibody of Claim 32, wherein said antibody is a polyclonal antibody.

34. The antibody of Claim 33, wherein said antibody is a chimeric antibody.

35. The antibody of any of Claims 31-34 detectably labeled.

36. The antibody of Claim 35, wherein said detectable label comprises an enzyme, a chemical which fluoresces, or a radioactive isotope.

37. A cloning vector comprising an isolated nucleic acid residue of either of Claims 24 or 25, and an origin of replication.

38. The cloning vector of Claim 37, wherein said cloning vector is selected from the group consisting of *E. coli*, bacteriophages, plasmids, and pUC plasmid derivatives.

39. The cloning vector of Claim 37, wherein bacteriophages further comprise lambda derivatives, plasmids further comprise pBR322 derivatives, and pUC plasmid derivatives further comprise pGEX vectors, or pmal-c, pFLAG.

40. An expression vector comprising an isolated nucleic acid molecule of either of Claims 24 or 25, operatively associated with a promoter.

41. The expression vector of Claim 40, wherein said promoter is selected from the group consisting of the immediate early promoters of hCMV, early promoters of SV40, early promoters of adenovirus, early promoters of vaccinia, early promoters of polyoma, late promoters of SV40, late promoters of adenovirus, late promoters of vaccinia, late promoters of polyoma, the *lac* the *trp* system, the *TAC* system, the *TRC* system, the major operator and promoter regions of phage lambda, control regions of fd coat protein, 3-phosphoglycerate kinase promoter, acid phosphatase promoter, and promoters of yeast α mating factor.

42. A unicellular host transformed with an expression vector of Claim 40.

43. The unicellular host of Claim 42, wherein said host is selected from the group

consisting of *E. coli*, Pseudonomas, Bacillus, Strepomyces, yeast, CHO, R1.1, B-W, L-M, COS1, COS7, BSC1, BSC40, BMT10 and Sf9 cells.

44. A method of producing a mutant cation channel protein comprising an amino acid sequence of SEQ ID NO:16, or conserved variants thereof, comprising the steps of:

a) culturing a unicellular host of Claim 42 under conditions that provide for expression of said mutant cation channel protein; and

b) recovering said mutant cation channel protein from said unicellular host.

45. A method of screening for compounds which selectively bind to a potassium ion channel protein comprising:

(a) complexing a functional two-transmembrane-domain-type potassium ion channel protein to a solid support;

(b) ontacting the complexed protein/solid support with an aqueous solution said solution containing a compound that is being screened for the ability to selectively bind to the ion channel protein;

(c) determining whether the compound selectively binds to the ion channel protein with the provisoes that the potassium ion channel protein is in the form of a tetrameric protein; and,

when the protein is mutated to correspond to the agitoxin2 docking site of a Shaker K^+ channel protein by substituting amino acid residues permitting the mutated protein to bind agitoxin2, the protein will bind agitoxin 2 while bound to the solid support, said substituting of residues being within the 36 amino acid domain defined by -25 to +5 of the selectivity filter where the 0 residue is either the phenylalanine or the tyrosine of the filter's signature sequence selected from the group consisting of glycine-phenylalanine-glycine or glycine-tyrosine-glycine.

46. A method of claim 45 wherein the solid supports are selected from the group

comprising: cobalt, insoluble polystyrene beads, PVDF, and polyethylene glycol.

47. A method of claim 45 wherein the two-transmembrane-domain-type ion channel protein is a prokaryote.

48. A method of claim 45, wherein the two-transmembrane-domain-type ion channel protein is from *Steptomyces lividans*.

49. A method of claim 45 wherein the two-transmembrane-domain-type ion channel protein is KcsA.

50. A method of claim 45 wherein the two-transmembrane-domain-type ion channel protein is mutated from a wild-type protein.

51. A method of claim 50 where the mutation is within the 36 amino acid domain defined by -25 to +5 of the selectivity filter where the 0 residue is either the phenylalanine or the tyrosine of the filter's signature sequence selected from the group consisting of glycine-phenylalanine-glycine or glycine-tyrosine-glycine.

52. A method of claim 50 wherein the mutation deletes a subsequence of the native amino acid sequence and replaces that the native with a subseqeunce from the corresponding domain of a second and different ion channel protein.

53. A method of claim 52 wherein the second ion channel protein is from a eukaryote.

54. A method claim 45 wherein the aqueous solution comprises a non-ionic detergent.

55. A non-natural and functional two-transmembrane-domain-type potassium ion channel protein wherein the non-natural protein is mutated in its amino acid sequence from a corresponding natural protein whereby the mutation does not prevent the non-natural protein from binding agitoxin2 when the non-natural protein is further mutated to correspond to the agitoxin2 docking site of a Shaker K^+ channel protein said docking site created by substituting amino acid residues selected from within the 36 amino acid domain defined by -25 to +5 of the Shaker

K^+ selectivity filter where the 0 residue is either the phenylalanine or the tyrosine of the filter's signature sequence selected from the group consisting of glycine-phenylalanine-glycine or glycine-tyrosine-glycine.

56. A non-natural protein of claim 55 wherein the protein binds to a channel blocking protein toxin with at least a 10 fold increase in affinity over the native ion channel.

57. A non-natural protein of claim 55 wherein the natural protein is the KcsA from *Streptomyces lividans*.

58. A method of assessing the adequacy of the structural conformation of a two-transmembrane-domain-type potassium ion channel protein for high through put assays comprising the steps of:

(a) complexing a two-transmembrane-domain-type potassium ion channel protein having a tetrameric form to a non-lipid solid support under aqueous conditions;

(b) contacting the complexed two-transmembrane-domain-type potassium ion channel protein with a substance known to bind to the two-transmembrane-domain-type potassium ion channel protein when bound to lipid membrane wherein the substance also modulates potassium ion flow in that channel protein; and,

(c) detecting the binding of the substance to the complexed two-transmembrane-domain-type potassium ion channel protein.

59. A method of claim 58 wherein the two-transmembrane-domain-type potassium ion channel protein is mutated from a wild type two-transmembrane-domain-type potassium ion channel protein by substitution of amino acids.

60. A method of claim 58 wherein the contacting is done in the presence of a non-ionic detergent.

60. A method of claim 58 where in the substance is a channel blocker.

62. A method of claim 58 wherein the substance is a toxin.

63. A prescreening method for identifying potential modulators of potassium ion channel function comprising:

(a) binding a soluble potassium ion channel protein to a solid support where the ion channel has the scaffold of a two-transmembrane-domain-type potassium ion channel and has a tetrameric confirmation;

(b) contacting the soluble potassium ion channel protein of step i with a compound in an aqueous solution; and,

(c) determining the binding of the compound to the soluble potassium ion channel protein.

64. A method of claim 63 wherein the contacting takes place in the presence of a detergent.

65. A method of claim 63 wherein the ion channel can pass potassium ions when expressed in a cell.

66. A method of claim 63 which further comprises the contacting of the compound to cell expressing a two-transmembrane-domain-type potassium ion channel protein said cell cultured in an aqueous media containing potassium and determining modulation of potassium flow between the inside of the cell and the media.

67. A column comprising a solid support having bound thereto an ion channel having the scaffold of a two-transmembrane-domain-type potassium ion channel and having a tetrameric confirmation.

68. A column of claim 25 wherein the ion channel is a non-natural and functional two-transmembrane-domain-type potassium ion channel protein wherein the

non-natural protein is mutated in its amino acid sequence from a corresponding natural protein whereby the mutation does not prevent the non-natural protein from binding agitoxin2 when the non-natural protein is further mutated to correspond to the agitoxin2 docking site of a Shaker K^+ channel protein said docking site created by substituting amino acid residues selected from within the 36 amino acid domain defined by -25 to +5 of the Shaker K^+ selectivity filter where the 0 residue is either the phenylalanine or the tyrosine of the filter's signature sequence selected from the group consisting of glycine-phenylalanine-glycine or glycine-tyrosine-glycine.